

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/517, 155A
Source: JFWP
Date Processed by STIC: 08/14/2006

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 08/14/2006

PATENT APPLICATION: US/10/517,155A

TIME: 13:25:45

Input Set : A:\211080011U6.TXT

Output Set: N:\CRF4\08142006\J517155A.raw

4 <110> APPLICANT: Chang, Chawnshang
 6 <120> TITLE OF INVENTION: Androgen Receptor Coregulators
 9 <130> FILE REFERENCE: 21108.0011U6
 11 <140> CURRENT APPLICATION NUMBER: 10/517,155A
 C--> 12 <141> CURRENT FILING DATE: 2004-12-06
 14 <150> PRIOR APPLICATION NUMBER: PCT/US03/17937
 15 <151> PRIOR FILING DATE: 2003-06-06
 17 <150> PRIOR APPLICATION NUMBER: US 60/387,087
 18 <151> PRIOR FILING DATE: 2002-06-06
 20 <160> NUMBER OF SEQ ID NOS: 47
 22 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1721
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Homo sapien
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (40)...(1464)
 33 <220> FEATURE:
 34 <221> NAME/KEY: misc_feature
 35 <222> LOCATION: (1120)...(1452)
 36 <223> OTHER INFORMATION: Coding sequence and polypeptide region for the
 37 C-terminal domain
 39 <220> FEATURE:
 40 <221> NAME/KEY: misc_feature
 41 <222> LOCATION: (697)...(834)
 42 <223> OTHER INFORMATION: Coding sequence and polypeptide region which may
 43 form a cystein-rich RING finger motif
 45 <220> FEATURE:
 46 <221> NAME/KEY: misc_feature
 47 <222> LOCATION: (964)...(1089)
 48 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
 49 cystein-rich B box like structure
 51 <400> SEQUENCE: 1
 52 ggtctctggt ctcccctctc tgagcactct gaggtcctt atg tcg tca gaa gat 54
 53 Met Ser Ser Glu Asp
 54 1 5
 56 cga gaa gct cag gag gat gaa ttg ctg gcc ctg gca agt att tac gat 102
 57 Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu Ala Ser Ile Tyr Asp
 58 10 15 20
 60 gga gat gaa ttt aga aaa gca gag tct gtc caa ggt gga gaa acc agg 150
 61 Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln Gly Gly Glu Thr Arg
 62 25 30 35

CP9-6)

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64 atc tat ttg gat ttg cca cag aat ttc aag ata ttt gtg agc ggc aat      198
65 Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile Phe Val Ser Gly Asn
66          40          45          50
68 tca aat gag tgt ctc cag aat agt ggc ttt gaa tac acc att tgc ttt      246
69 Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu Tyr Thr Ile Cys Phe
70          55          60          65
72 ctg cct cca ctt gtg ctg aac ttt gaa ctg cca cca gat tat cca tcc      294
73 Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro Pro Asp Tyr Pro Ser
74 70          75          80          85
76 tct tcc cca cct tca ttc aca ctt agt ggc aaa tgg ctg tca cca act      342
77 Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys Trp Leu Ser Pro Thr
78          90          95          100
80 cag cta tct gct cta tgc aag cac tta gac aac cta tgg gaa gaa cac      390
81 Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn Leu Trp Glu Glu His
82          105          110          115
84 cgt ggc agc gtg gtc ctg ttt gcc tgg atg caa ttt ctt aag gaa gag      438
85 Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln Phe Leu Lys Glu Glu
86          120          125          130
88 acc cta gca tac ttg aat att gtc tct cct ttt gag ctc aag att ggt      486
89 Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe Glu Leu Lys Ile Gly
90          135          140          145
92 tct cag aaa aaa gtg cag aga agg aca gct caa gct tct ccc aac aca      534
93 Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln Ala Ser Pro Asn Thr
94 150          155          160          165
96 gag cta gat ttt gga gga gct gct gga tct gat gta gac caa gag gaa      582
97 Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp Val Asp Gln Glu Glu
98          170          175          180
100 att gtg gat gag aga gca gtg cag gat gtg gaa tca ctg tca aat ctg      630
101 Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu Ser Leu Ser Asn Leu
102          185          190          195
104 atc cag gaa atc ttg gac ttt gat caa gct cag cag ata aaa tgc ttt      678
105 Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln Gln Ile Lys Cys Phe
106          200          205          210
108 aat agt aaa ttg ttc ctg tgc agt atc tgt ttc tgt gag aag ctg ggt      726
109 Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe Cys Glu Lys Leu Gly
110          215          220          225
112 agt gaa tgc atg tac ttc ttg gag tgc agg cat gtg tac tgc aaa gcc      774
113 Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His Val Tyr Cys Lys Ala
114 230          235          240          245
116 tgt ctg aag gac tac ttt gaa atc cag atc aga gat ggc cag gtt caa      822
117 Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg Asp Gly Gln Val Gln
118          250          255          260
120 tgc ctc aac tgc cca gaa cca aag tgc cct tcg gtg gcc act cct ggt      870
121 Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser Val Ala Thr Pro Gly
122          265          270          275
124 cag gtc aaa gag tta gtg gaa gca gag tta ttt gcc cgt tat gac cgc      918
125 Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe Ala Arg Tyr Asp Arg
126          280          285          290
128 ctt ctc ctc cag tcc tcc ttg gac ctg atg gca gat gtg gtg tac tgc      966

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129 Leu Leu Leu Gln Ser Ser Leu Asp Leu Met Ala Asp Val Val Tyr Cys
130      295                      300                      305
132 ccc cgg ccg tgc tgc cag ctg cct gtg atg cag gaa cct ggc tgc acc      1014
133 Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln Glu Pro Gly Cys Thr
134 310                      315                      320                      325
136 atg ggt atc tgc tcc agc tgc aat ttt gcc ttc tgt act ttg tgc agg      1062
137 Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe Cys Thr Leu Cys Arg
138                      330                      335                      340
140 ttg acc tac cat ggg gtc tcc cca tgt aag gtg act gca gag aaa tta      1110
141 Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val Thr Ala Glu Lys Leu
142                      345                      350                      355
144 atg gac tta cga aat gaa tac ctg caa gcg gat gag gct aat aaa aga      1158
145 Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp Glu Ala Asn Lys Arg
146                      360                      365                      370
148 ctt ttg gat caa agg tat ggt aag aga gtg att cag aag gca ctg gaa      1206
149 Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile Gln Lys Ala Leu Glu
150                      375                      380                      385
152 gag atg gaa agt aag gag tgg cta gag aag aac tca aag agc tgc cca      1254
153 Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn Ser Lys Ser Cys Pro
154 390                      395                      400                      405
156 tgt tgt gga act ccc ata gag aaa tta gac gga tgt aac aag atg aca      1302
157 Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly Cys Asn Lys Met Thr
158                      410                      415                      420
160 tgt act ggc tgt atg caa tat ttc tgt tgg att tgc atg ggt tct ctc      1350
161 Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile Cys Met Gly Ser Leu
162                      425                      430                      435
164 tct aga gca aac cct tac aaa cat ttc aat gac cct ggt tca cca tgt      1398
165 Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp Pro Gly Ser Pro Cys
166                      440                      445                      450
168 ttt aac cgg ctg ttt tat gct gtg gat gtt gac gac gat att tgg gaa      1446
169 Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp Asp Asp Ile Trp Glu
170                      455                      460                      465
172 gat gag gta gaa gac tag ttaactactg ctcaagatat ttaactactg      1494
173 Asp Glu Val Glu Asp *
174 470
176 ctcaagatat ggaagtggat tgtttttccc taatcttccg tcaagtacac aaagtaactt      1554
177 tgcgggatatt ttaggggtact attcattcac tcttcctgcg tagaagatat ggaagaacga      1614
178 ggtttatatt ttcatgtggt actactgaag aaggtgcatt gatacathtt taaatgtaag      1674
179 ttgagaaaaa ttataagcc aaaggttcag aaaattaaac tacagaa      1721
181 <210> SEQ ID NO: 2
182 <211> LENGTH: 474
183 <212> TYPE: PRT
184 <213> ORGANISM: Homo sapien
186 <400> SEQUENCE: 2
187 Met Ser Ser Glu Asp Arg Glu Ala Gln Glu Asp Glu Leu Leu Ala Leu
188 1      5      10      15
189 Ala Ser Ile Tyr Asp Gly Asp Glu Phe Arg Lys Ala Glu Ser Val Gln
190      20      25      30
191 Gly Gly Glu Thr Arg Ile Tyr Leu Asp Leu Pro Gln Asn Phe Lys Ile

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192          35          40          45
193 Phe Val Ser Gly Asn Ser Asn Glu Cys Leu Gln Asn Ser Gly Phe Glu
194          50          55          60
195 Tyr Thr Ile Cys Phe Leu Pro Pro Leu Val Leu Asn Phe Glu Leu Pro
196 65          70          75          80
197 Pro Asp Tyr Pro Ser Ser Ser Pro Pro Ser Phe Thr Leu Ser Gly Lys
198          85          90          95
199 Trp Leu Ser Pro Thr Gln Leu Ser Ala Leu Cys Lys His Leu Asp Asn
200          100          105          110
201 Leu Trp Glu Glu His Arg Gly Ser Val Val Leu Phe Ala Trp Met Gln
202          115          120          125
203 Phe Leu Lys Glu Glu Thr Leu Ala Tyr Leu Asn Ile Val Ser Pro Phe
204          130          135          140
205 Glu Leu Lys Ile Gly Ser Gln Lys Lys Val Gln Arg Arg Thr Ala Gln
206 145          150          155          160
207 Ala Ser Pro Asn Thr Glu Leu Asp Phe Gly Gly Ala Ala Gly Ser Asp
208          165          170          175
209 Val Asp Gln Glu Ile Val Asp Glu Arg Ala Val Gln Asp Val Glu
210          180          185          190
211 Ser Leu Ser Asn Leu Ile Gln Glu Ile Leu Asp Phe Asp Gln Ala Gln
212          195          200          205
213 Gln Ile Lys Cys Phe Asn Ser Lys Leu Phe Leu Cys Ser Ile Cys Phe
214          210          215          220
215 Cys Glu Lys Leu Gly Ser Glu Cys Met Tyr Phe Leu Glu Cys Arg His
216 225          230          235          240
217 Val Tyr Cys Lys Ala Cys Leu Lys Asp Tyr Phe Glu Ile Gln Ile Arg
218          245          250          255
219 Asp Gly Gln Val Gln Cys Leu Asn Cys Pro Glu Pro Lys Cys Pro Ser
220          260          265          270
221 Val Ala Thr Pro Gly Gln Val Lys Glu Leu Val Glu Ala Glu Leu Phe
222          275          280          285
223 Ala Arg Tyr Asp Arg Leu Leu Gln Ser Ser Leu Asp Leu Met Ala
224          290          295          300
225 Asp Val Val Tyr Cys Pro Arg Pro Cys Cys Gln Leu Pro Val Met Gln
226 305          310          315          320
227 Glu Pro Gly Cys Thr Met Gly Ile Cys Ser Ser Cys Asn Phe Ala Phe
228          325          330          335
229 Cys Thr Leu Cys Arg Leu Thr Tyr His Gly Val Ser Pro Cys Lys Val
230          340          345          350
231 Thr Ala Glu Lys Leu Met Asp Leu Arg Asn Glu Tyr Leu Gln Ala Asp
232          355          360          365
233 Glu Ala Asn Lys Arg Leu Leu Asp Gln Arg Tyr Gly Lys Arg Val Ile
234          370          375          380
235 Gln Lys Ala Leu Glu Glu Met Glu Ser Lys Glu Trp Leu Glu Lys Asn
236 385          390          395          400
237 Ser Lys Ser Cys Pro Cys Cys Gly Thr Pro Ile Glu Lys Leu Asp Gly
238          405          410          415
239 Cys Asn Lys Met Thr Cys Thr Gly Cys Met Gln Tyr Phe Cys Trp Ile
240          420          425          430

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241 Cys Met Gly Ser Leu Ser Arg Ala Asn Pro Tyr Lys His Phe Asn Asp
242         435                     440                     445
243 Pro Gly Ser Pro Cys Phe Asn Arg Leu Phe Tyr Ala Val Asp Val Asp
244         450                     455                     460
245 Asp Asp Ile Trp Glu Asp Glu Val Glu Asp
246 465                     470
248 <210> SEQ ID NO: 3
249 <211> LENGTH: 1335
250 <212> TYPE: DNA
251 <213> ORGANISM: Homo sapien
253 <220> FEATURE:
254 <221> NAME/KEY: CDS
255 <222> LOCATION: (1)...(1335)
257 <220> FEATURE:
258 <221> NAME/KEY: misc_feature
259 <222> LOCATION: (750)...(1332)
260 <223> OTHER INFORMATION: Coding sequence and polypeptide region for the
261     C-terminal binding domain
263 <220> FEATURE:
264 <221> NAME/KEY: misc_feature
265 <222> LOCATION: (631)...(783)
266 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
267     cystein rich LIM motif
269 <220> FEATURE:
270 <221> NAME/KEY: misc_feature
271 <222> LOCATION: (808)...(996)
272 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
273     cystein rich LIM motif
275 <220> FEATURE:
276 <221> NAME/KEY: misc_feature
277 <222> LOCATION: (985)...(1137)
278 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
279     cystein rich LIM motif
281 <220> FEATURE:
282 <221> NAME/KEY: misc_feature
283 <222> LOCATION: (1162)...(1314)
284 <223> OTHER INFORMATION: Coding sequence and polypeptide region for a
285     cystein rich LIM motif
287 <400> SEQUENCE: 3
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289 Met Pro Arg Ser Gly Ala Pro Lys Glu Arg Pro Ala Glu Pro Leu Thr
290 1         5         10         15
292 cct ccc cca tcc tat ggc cac cag cca aca ggg cag tct ggg gag tct      96
293 Pro Pro Pro Ser Tyr Gly His Gln Pro Thr Gly Gln Ser Gly Glu Ser
294         20         25         30
296 tca gga gcc tcg ggg gac aag gac cac ctg tac agc acg gta tgc aag      144
297 Ser Gly Ala Ser Gly Asp Lys Asp His Leu Tyr Ser Thr Val Cys Lys
298         35         40         45
300 cct cgg tcc cca aag cct gca gcc ccg gcc gcc cct cca ttc tcc tct      192

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RAW SEQUENCE LISTING ERROR SUMMARY DATE: 08/14/2006
PATENT APPLICATION: US/10/517,155A TIME: 13:25:46

Input Set : A:\211080011U6.TXT
Output Set: N:\CRF4\08142006\J517155A.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,15,17,18,20,21,23,24,25,26,27
Seq#:11; Xaa Pos. 28,30,31
Seq#:12; Xaa Pos. 2,3,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,22,23,25
Seq#:12; Xaa Pos. 26,28,29,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46
Seq#:12; Xaa Pos. 48,49

VERIFICATION SUMMARY

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L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1028 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0

M:341 Repeated in SeqNo=11

L:1044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12 after pos.:0

M:341 Repeated in SeqNo=12